

Supplementary figures for “Differential chromatin marking of introns and expressed exons by H3K36me3”

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Content: 3 supplementary figures

Supplementary tables are available separately with the on-line version of the article

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Supplementary Figure 1. Patterns of histone methylations across *C. elegans* genes

(a) Mean log₂ ChIP signal of indicated histone modification, plotted across all genes (black), top10 genes (red) and bottom10 genes (blue) aligned at the first and last nucleotides (0% and 100%) and extended with 1kb upstream and downstream sequence.

(b) Similar plots to (a) but limited to genes of length 1.9 - 2.1kb. Top10 and bottom10 are genes in the top and bottom 10% of expression level based on microarray expression profiling of the ChIP samples.

Supplementary Figure 2. H3K36me3 is enriched across *C. elegans* exonic chromatin

Mean log₂ ChIP signals for (a) H3K36me3 (b) H3K4me3 and (c) H3K9me3 across intron/exon and exon/intron boundaries where introns are at least 400bp and exons at least 80bp, excluding first and last exons. Black, exons of all genes; red, top10 genes; blue, bottom10 genes. In the gene model, thin grey lines represent 400bp of intron sequence, blue boxes 40bp of exon sequence, and thick grey lines the centres of exons that vary in length.

Supplementary Figure 3. Histone modification signals across long exons. Mean log₂ ChIP signals or tag counts across exons of length 900-1000bp flanked on both sides by introns of ≥ 500 bp. (a-c) *C. elegans*: (a) H3K36me3 (b) H3K4me3 (c) H3K9me3. (d, e) mouse: (d) H3K36me3 (e) H3K4me3. (f-h) human: (f) H3K36me3 (g) H3K4me3 (h) H3K27me1. In diagrams below plots, black boxes represent exons and black lines introns.





